

SEQUENCE LISTING

<110> Fox, Brian
 Holloway, James L.

<120> ADIPOCYTE COMPLMENT RELATED PROTEIN
 ZACRP13

<130> 00-96

<150> US 60/253,924
 <151> 2000-11-29

<160> 7

<170> FastSEQ for Windows Version 3.0

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (2).. (1381)

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 1 5 10 15

gtt gct gga cct cca gca cac ccc agg ccc cca gaa gaa gtg ggg cct 97
 Val Ala Gly Pro Pro Ala His Pro Arg Pro Pro Glu Glu Val Gly Pro
 20 25 30

cct ggt gca cca ggt tta cca caa tat aca gga gaa ata agt gaa atg 145
 Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr Gly Glu Ile Ser Glu Met
 35 40 45

aca aaa tgc ccc tgt cct gat ata gaa agg tca gcc ttt act gtg aag 193
 Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys
 50 55 60

ctc	agt	gga	aaa	ctt	cct	ctt	cct	ttc	aag	ccc	atc	atc	ttc	aca	ggg	241
Leu	Ser	Gly	Lys	Leu	Pro	Leu	Pro	Phe	Lys	Pro	Ile	Ile	Phe	Thr	Gly	
65				70					75				80			
gtc	ctg	tac	aat	gcc	cag	agg	gat	tta	aag	gag	gcc	atg	gga	gtc	ttt	289
Val	Leu	Tyr	Asn	Ala	Gln	Arg	Asp	Leu	Lys	Glu	Ala	Met	Gly	Val	Phe	
85								90					95			
gct	tgc	agg	gtg	cct	ggg	aat	tac	tac	tcc	agc	ttt	gat	gtt	gag	ctg	337
Ala	Cys	Arg	Val	Pro	Gly	Asn	Tyr	Tyr	Ser	Ser	Phe	Asp	Val	Glu	Leu	
100							105					110				
cat	cat	tgc	aag	gtg	aat	att	tgg	cta	atg	agg	aag	caa	att	ttg	gct	385
His	His	Cys	Lys	Val	Asn	Ile	Trp	Leu	Met	Arg	Lys	Gln	Ile	Leu	Ala	
115							120					125				
aat	aag	gaa	gaa	att	tct	aag	cag	caa	agc	att	caa	gag	gtg	act	tgg	433
Asn	Lys	Glu	Glu	Ile	Ser	Lys	Gln	Gln	Ser	Ile	Gln	Glu	Val	Thr	Trp	
130							135					140				
gtg	ctg	tta	aag	gca	ttc	agt	ttc	ata	agg	gag	gca	gag	cat	aag	agt	481
Val	Leu	Leu	Lys	Ala	Phe	Ser	Phe	Ile	Arg	Glu	Ala	Glu	His	Lys	Ser	
145							150				155		160			
tca	gaa	aat	ttg	cac	cct	gac	aat	gtg	ata	aaa	aag	aaa	aac	cca	ttt	529
Ser	Glu	Asn	Leu	His	Pro	Asp	Asn	Val	Ile	Lys	Lys	Lys	Asn	Pro	Phe	
165							170					175				
tct	gag	ggg	aaa	ttc	aag	ctg	gct	gca	gaa	att	tgc	ata	tgt	aat	gag	577
Ser	Glu	Gly	Lys	Phe	Lys	Leu	Ala	Ala	Glu	Ile	Cys	Ile	Cys	Asn	Glu	
180							185					190				
gag	ctg	aat	gtt	aat	cct	caa	gac	aat	ggg	gaa	aat	atc	tcc	tgg	aca	625
Glu	Leu	Asn	Val	Asn	Pro	Gln	Asp	Asn	Gly	Glu	Asn	Ile	Ser	Trp	Thr	
195							200					205				
tgt	cag	agg	tct	tca	cag	cag	tcc	atc	aaa	tca	ctg	gcc	tgg	agg	cct	673
Cys	Gln	Arg	Ser	Ser	Gln	Gln	Ser	Ile	Lys	Ser	Leu	Ala	Trp	Arg	Pro	
210							215					220				
agg	aga	aaa	tgg	ttt	tgt	ggg	aca	ggc	cca	ggg	tcc	ctg	tgc	tgt	gtg	721

Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val			
225	230	235	240
cag cct aga gac ttg gtg ccc tgt gtc cca gtt aat tca gct gtg gct			769
Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala			
245	250	255	
tca gag ggt gca agc ccc aag cct tgg cag ctt cca agt ggt gtt gag			817
Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu			
260	265	270	
cct gtg ggt gca aag aag tca aga att gag gtt tgg gaa cct cca atc			865
Pro Val Gly Ala Lys Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile			
275	280	285	
aga ttt cag aag ata tat gga aac ccc tgg atg ccc agg cag aag ttt			913
Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe			
290	295	300	
gct gta ggg gtg ggg tcc tca tgg aga acc tct gca agg gta gta caa			961
Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln			
305	310	315	320
aag gga aat gtt ggg tgg gag ccc cca cac aga gtc ccc agt ggg gct			1009
Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala			
325	330	335	
cca tct agt aga gct gtg aga aga agt cca cca tcc tcc aga ctc cag			1057
Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln			
340	345	350	
aag ggt aga tcc act gac agc ttg cag cat gtg cct gaa aaa tcc aca			1105
Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr			
355	360	365	
gac act cag tgc cag cct gtg aaa gca gca ggg atg gag tct gta ccc			1153
Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro			
370	375	380	
tac aaa acc gta gtg gca gag ctg acc aag acc gtg gga atc tac ctc			1201
Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu			
385	390	395	400

ttg cat tgt cat gac ctg gac gtg aga cat gga gtc aaa aga gat cat 1249
 Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His
 405 410 415

ttt gga gct tta aga ttt gac tgc ccc act gga ttt cg^g act tat atg 1297
 Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met
 420 425 430

ggg ccc gta ccc ctt tgt ttt ggc caa ttt ttt cca ttt gga act gcc 1345
 Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala
 435 440 445

gta ttt acc caa tgc ctg tac ctc cat tgt atg tag 1381
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 450 455

<210> 2
 <211> 459
 <212> PRT
 <213> Homo sapiens

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 Val Ala Gly Pro Pro Ala His Pro Arg Pro Pro Glu Glu Val Gly Pro
 20 25 30
 Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr Gly Glu Ile Ser Glu Met
 35 40 45
 Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg Ser Ala Phe Thr Val Lys
 50 55 60
 Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys Pro Ile Ile Phe Thr Gly
 65 70 75 80
 Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys Glu Ala Met Gly Val Phe
 85 90 95
 Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser Ser Phe Asp Val Glu Leu
 100 105 110
 His His Cys Lys Val Asn Ile Trp Leu Met Arg Lys Gln Ile Leu Ala
 115 120 125
 Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser Ile Gln Glu Val Thr Trp
 130 135 140
 Val Leu Leu Lys Ala Phe Ser Phe Ile Arg Glu Ala Glu His Lys Ser
 145 150 155 160

Q1 Q2 Q3 Q4 Q5 Q6 Q7 Q8 Q9 Q10 Q11 Q12 Q13 Q14 Q15 Q16 Q17 Q18 Q19 Q20

Ser Glu Asn Leu His Pro Asp Asn Val Ile Lys Lys Lys Asn Pro Phe
 165 170 175
 Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu Ile Cys Ile Cys Asn Glu
 180 185 190
 Glu Leu Asn Val Asn Pro Gln Asp Asn Gly Glu Asn Ile Ser Trp Thr
 195 200 205
 Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys Ser Leu Ala Trp Arg Pro
 210 215 220
 Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro Gly Ser Leu Cys Cys Val
 225 230 235 240
 Gln Pro Arg Asp Leu Val Pro Cys Val Pro Val Asn Ser Ala Val Ala
 245 250 255
 Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln Leu Pro Ser Gly Val Glu
 260 265 270
 Pro Val Gly Ala Lys Lys Ser Arg Ile Glu Val Trp Glu Pro Pro Ile
 275 280 285
 Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp Met Pro Arg Gln Lys Phe
 290 295 300
 Ala Val Gly Val Gly Ser Ser Trp Arg Thr Ser Ala Arg Val Val Gln
 305 310 315 320
 Lys Gly Asn Val Gly Trp Glu Pro Pro His Arg Val Pro Ser Gly Ala
 325 330 335
 Pro Ser Ser Arg Ala Val Arg Arg Ser Pro Pro Ser Ser Arg Leu Gln
 340 345 350
 Lys Gly Arg Ser Thr Asp Ser Leu Gln His Val Pro Glu Lys Ser Thr
 355 360 365
 Asp Thr Gln Cys Gln Pro Val Lys Ala Ala Gly Met Glu Ser Val Pro
 370 375 380
 Tyr Lys Thr Val Val Ala Glu Leu Thr Lys Thr Val Gly Ile Tyr Leu
 385 390 395 400
 Leu His Cys His Asp Leu Asp Val Arg His Gly Val Lys Arg Asp His
 405 410 415
 Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr Gly Phe Arg Thr Tyr Met
 420 425 430
 Gly Pro Val Pro Leu Cys Phe Gly Gln Phe Phe Pro Phe Gly Thr Ala
 435 440 445
 Val Phe Thr Gln Cys Leu Tyr Leu His Cys Met
 450 455

<210> 3

<211> 1377

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate polynucleotide encoding a polypeptide
of SEQ ID NO:2

<221> variation

<222> (1)...(1377)

<223> Each n is independently A, T, G, or C.

<221> misc_feature

<222> (1)...(1377)

<223> n = A,T,C or G

<400> 3

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ccngcncayc cnmgncncc ngargargtn ggnccncng gngcnccnng nytnccncar	120
tayacngng arathwsnga ratgacnaar tgycntgyc cngayathga rmgnwsngcn	180
ttyacngtna arytnwsngg naarytnccn ytnccnttya arccnathat httyacnggn	240
gtnytntaya aygcncarng ngayytnaar gargnatgg gngtnttygc ntgymngntn	300
ccnggnaayt aytawwsnws nttygaygtn garytncayc aytgyaargt naayathtgg	360
ytnatgmna arcarathyt ngcnaayaar gargarathw snaarcarca rwsnathcar	420
gargtnacnt gggtnytnyt naargcntty wsnttyathm gngargcnga rcayaarwsn	480
wsnaraayy tncayccnga yaaygtnath aaraaraara ayccnttyws ngarggnaar	540
ttyaarytrng cngcngarat htgyathtgy aaygargary tnaaygtnaa yccncargay	600
aayggngara ayathwsntg gacntgycar mgnwsnwsnc arcarwsnat haarwsnytn	660
gcntggmgnc cnmgmgnnaa rtggattyg ggnacnggnc cnggnwsnyt ntgytgygtn	720
carccnmngrg ayytngtnc ntgygtncn gtnaaywsng cngtngcnws ngarggngcn	780
wsnccnaarc cntggcaryt nccnwsnngn gtngarccng tnggngcnaa raarwsnmgn	840
athgargtn gggarcncc nathmgntt caraaratht ayygnaaycc ntggatgccn	900
mgncaraart tygcngtngg ntnggnwsn wsntggmgn cnwsngcnmg ngtngtnca	960
aarggnaayg tnggntggga rccnccnca mngtnccnw snggngcncc nwsnwsnmgn	1020
gcngtnmgnm gnwsnccncc nwsnwsnmgn ytncaarg gnmgnwsnac ngaywsnytn	1080
carcaygtnc cngaraarws nacngayacn cartgycarc cngtnaargc ngcnggnatg	1140
garwsngtnc cntayaarac ntngtngcn garytnacna aracngtngg nathtayytn	1200
ytncaytgyc ayygatyng aytngmgnac ggnngtnaarm gngaycayt yggngcnytn	1260
mgnttygaty gycnacngg nttymgnacn tayatggnc cngtnccnyt ntgytgyggn	1320
carttattytc ctttgggnac ngcngtnnyt acncartgyy tntayytnca ytgyatg	1377

<210> 4

<211> 31

<212> PRT

<213> Artificial Sequence

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<223> Aromatic motif

<221> VARIANT

<222> (2)...(6)

<223> Each Xaa is any amino acid residue

<221> VARIANT

<222> (7)...(7)

<223> Xaa is asparagine or aspartic acid

<221> VARIANT

<222> (8)...(11)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (12)...(12)

<223> Xaa is phenylalanine, tyrosine, tryptophan, or leucine

<221> VARIANT

<222> (13)...(18)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (20)...(24)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (26)...(26)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (28)...(31)

<223> Each Xaa is independently any amino acid residue

<400> 4

Phe Xaa
 1 5 10 15

Xaa Xaa Phe Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Xaa Xaa Xaa
 20 25 30

<210> 5
 <211> 1731
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1731)

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1	5	10	15		
aaa tgc tgc att gga gag atg ggg tac atg cga gtg aca atg gga aga					96
Lys Cys Cys Ile Gly Glu Met Gly Tyr Met Arg Val Thr Met Gly Arg					
20	25	30			
gtt ggt agc tgg aga gaa ctg gga aag cct tca ggc atc tgg gaa atg					144
Val Gly Ser Trp Arg Glu Leu Gly Lys Pro Ser Gly Ile Trp Glu Met					
35	40	45			
gct ggg gat aca gag gtg aag aag aca ggg ttt ctt cag gaa ctc act					192
Ala Gly Asp Thr Glu Val Lys Lys Thr Gly Phe Leu Gln Glu Leu Thr					
50	55	60			
ttc cag cag gag cct ggc atc tcc tcc tct cct tgc tcc cgc tct					240
Phe Gln Gln Glu Pro Gly Ile Ser Ser Pro Ser Cys Ser Arg Ser					
65	70	75	80		
tgc cat gtg aca cca cct gct cca cct gca tct tct gcc ata att gta					288
Cys His Val Thr Pro Pro Ala Pro Pro Ala Ser Ser Ala Ile Ile Val					
85	90	95			
aga ttc ctg agg ccc tca cca gaa gca gat gcc agc agc atg ctt att					336
Arg Phe Leu Arg Pro Ser Pro Glu Ala Asp Ala Ser Ser Met Leu Ile					
100	105	110			
gca cag tct gta gaa ccg ata gtg gtc ata cct gtc tta ata acg gca					384
Ala Gln Ser Val Glu Pro Ile Val Val Ile Pro Val Leu Ile Thr Ala					
115	120	125			
gtc att gag cat gta gaa gtt gct gga cct cca gca cac ccc agg ccc					432

Val	Ile	Glu	His	Val	Glu	Val	Ala	Gly	Pro	Pro	Ala	His	Pro	Arg	Pro	
130				135					140							
cca	gaa	gaa	gtg	ggg	cct	cct	ggt	gca	cca	ggt	tta	cca	caa	tat	aca	480
Pro	Glu	Glu	Val	Gly	Pro	Pro	Gly	Ala	Pro	Gly	Leu	Pro	Gln	Tyr	Thr	
145			150						155				160			
gga	gaa	ata	agt	gaa	atg	aca	aaa	tgc	ccc	tgt	cct	gat	ata	gaa	agg	528
Gly	Glu	Ile	Ser	Glu	Met	Thr	Lys	Cys	Pro	Cys	Pro	Asp	Ile	Glu	Arg	
165			170						175							
tca	gcc	ttt	act	gtg	aag	ctc	agt	gga	aaa	ctt	cct	ctt	cct	ttc	aag	576
Ser	Ala	Phe	Thr	Val	Lys	Leu	Ser	Gly	Lys	Leu	Pro	Leu	Pro	Phe	Lys	
180			185							190						
ccc	atc	atc	tcc	aca	ggg	gtc	ctg	tac	aat	gcc	cag	agg	gat	tta	aag	624
Pro	Ile	Ile	Phe	Thr	Gly	Val	Leu	Tyr	Asn	Ala	Gln	Arg	Asp	Leu	Lys	
195			200						205							
gag	gcc	atg	gga	gtc	ttt	gct	tgc	agg	gtg	cct	ggg	aat	tac	tac	tcc	672
Glu	Ala	Met	Gly	Val	Phe	Ala	Cys	Arg	Val	Pro	Gly	Asn	Tyr	Tyr	Ser	
210			215						220							
agc	ttt	gat	gtt	gag	ctg	cat	cat	tgc	aag	gtg	aat	att	tgg	cta	atg	720
Ser	Phe	Asp	Val	Glu	Leu	His	His	Cys	Lys	Val	Asn	Ile	Trp	Leu	Met	
225			230						235			240				
agg	aag	caa	att	ttg	gct	aat	aag	gaa	att	tct	aag	cag	caa	agc		768
Arg	Lys	Gln	Ile	Leu	Ala	Asn	Lys	Glu	Glu	Ile	Ser	Lys	Gln	Gln	Ser	
245			250						255							
att	caa	gag	gtg	act	tgg	gtg	ctg	tta	aag	gca	ttc	agt	ttc	ata	agg	816
Ile	Gln	Glu	Val	Thr	Trp	Val	Leu	Leu	Lys	Ala	Phe	Ser	Phe	Ile	Arg	
260			265						270							
gag	gca	gag	cat	aag	agt	tca	gaa	aat	ttg	cac	cct	gac	aat	gtg	ata	864
Glu	Ala	Glu	His	Lys	Ser	Ser	Glu	Asn	Leu	His	Pro	Asp	Asn	Val	Ile	
275			280						285							
aaa	aag	aaa	aac	cca	ttt	tct	gag	ggg	aaa	ttc	aag	ctg	gct	gca	gaa	912
Lys	Lys	Lys	Asn	Pro	Phe	Ser	Glu	Gly	Lys	Phe	Lys	Leu	Ala	Ala	Glu	
290			295						300							

att tgc ata tgt aat gag gag ctg aat gtt aat cct caa gac aat ggg Ile Cys Ile Cys Asn Glu Glu Leu Asn Val Asn Pro Gln Asp Asn Gly 305 310 315 320	960
gaa aat atc tcc tgg aca tgt cag agg tct tca cag cag tcc atc aaa Glu Asn Ile Ser Trp Thr Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys 325 330 335	1008
tca ctg gcc tgg agg cct agg aga aaa tgg ttt tgt ggg aca ggc cca Ser Leu Ala Trp Arg Pro Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro 340 345 350	1056
ggg tcc ctg tgc tgt gtg cag cct aga gac ttg gtg ccc tgt gtc cca Gly Ser Leu Cys Cys Val Gln Pro Arg Asp Leu Val Pro Cys Val Pro 355 360 365	1104
gtt aat tca gct gtg gct tca gag ggt gca agc ccc aag cct tgg cag Val Asn Ser Ala Val Ala Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln 370 375 380	1152
ctt cca agt ggt gtt gag cct gtg ggt gca aag aag tca aga att gag Leu Pro Ser Gly Val Glu Pro Val Gly Ala Lys Lys Ser Arg Ile Glu 385 390 395 400	1200
gtt tgg gaa cct cca atc aga ttt cag aag ata tat gga aac ccc tgg Val Trp Glu Pro Pro Ile Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp 405 410 415	1248
atg ccc agg cag aag ttt gct gta ggg gtg ggg tcc tca tgg aga acc Met Pro Arg Gln Lys Phe Ala Val Gly Val Gly Ser Ser Trp Arg Thr 420 425 430	1296
tct gca agg gta gta caa aag gga aat gtt ggg tgg gag ccc cca cac Ser Ala Arg Val Val Gln Lys Gly Asn Val Gly Trp Glu Pro Pro His 435 440 445	1344
aga gtc ccc agt ggg gct cca tct agt aga gct gtg aga aga agt cca Arg Val Pro Ser Gly Ala Pro Ser Ser Arg Ala Val Arg Arg Ser Pro 450 455 460	1392
cca tcc tcc aga ctc cag aag ggt aga tcc act gac agc ttg cag cat	1440

Pro Ser Ser Arg Leu Gln Lys Gly Arg Ser Thr Asp Ser Leu Gln His				
465	470	475	480	
gtg cct gaa aaa tcc aca gac act cag tgc cag cct gtg aaa gca gca				1488
Val Pro Glu Lys Ser Thr Asp Thr Gln Cys Gln Pro Val Lys Ala Ala				
485	490	495		
ggg atg gag tct gta ccc tac aaa acc gta gtg gca gag ctg acc aag				1536
Gly Met Glu Ser Val Pro Tyr Lys Thr Val Val Ala Glu Leu Thr Lys				
500	505	510		
acc gtg gga atc tac ctc ttg cat tgt cat gac ctg gac gtg aga cat				1584
Thr Val Gly Ile Tyr Leu Leu His Cys His Asp Leu Asp Val Arg His				
515	520	525		
gga gtc aaa aga gat cat ttt gga gct tta aga ttt gac tgc ccc act				1632
Gly Val Lys Arg Asp His Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr				
530	535	540		
gga ttt cgg act tat atg ggg ccc gta ccc ctt tgt ttt ggc caa ttt				1680
Gly Phe Arg Thr Tyr Met Gly Pro Val Pro Leu Cys Phe Gly Gln Phe				
545	550	555	560	
ttt cca ttt gga act gcc gta ttt acc caa tgc ctg tac ctc cat tgt				1728
Phe Pro Phe Gly Thr Ala Val Phe Thr Gln Cys Leu Tyr Leu His Cys				
565	570	575		
atg				1731
Met				

<210> 6
 <211> 577
 <212> PRT
 <213> Homo sapiens

<400> 6
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 20 25 30

Val Gly Ser Trp Arg Glu Leu Gly Lys Pro Ser Gly Ile Trp Glu Met
 35 40 45
 Ala Gly Asp Thr Glu Val Lys Lys Thr Gly Phe Leu Gln Glu Leu Thr
 50 55 60
 Phe Gln Gln Glu Pro Gly Ile Ser Ser Ser Pro Ser Cys Ser Arg Ser
 65 70 75 80
 Cys His Val Thr Pro Pro Ala Pro Pro Ala Ser Ser Ala Ile Ile Val
 85 90 95
 Arg Phe Leu Arg Pro Ser Pro Glu Ala Asp Ala Ser Ser Met Leu Ile
 100 105 110
 Ala Gln Ser Val Glu Pro Ile Val Val Ile Pro Val Leu Ile Thr Ala
 115 120 125
 Val Ile Glu His Val Glu Val Ala Gly Pro Pro Ala His Pro Arg Pro
 130 135 140
 Pro Glu Glu Val Gly Pro Pro Gly Ala Pro Gly Leu Pro Gln Tyr Thr
 145 150 155 160
 Gly Glu Ile Ser Glu Met Thr Lys Cys Pro Cys Pro Asp Ile Glu Arg
 165 170 175
 Ser Ala Phe Thr Val Lys Leu Ser Gly Lys Leu Pro Leu Pro Phe Lys
 180 185 190
 Pro Ile Ile Phe Thr Gly Val Leu Tyr Asn Ala Gln Arg Asp Leu Lys
 195 200 205
 Glu Ala Met Gly Val Phe Ala Cys Arg Val Pro Gly Asn Tyr Tyr Ser
 210 215 220
 Ser Phe Asp Val Glu Leu His His Cys Lys Val Asn Ile Trp Leu Met
 225 230 235 240
 Arg Lys Gln Ile Leu Ala Asn Lys Glu Glu Ile Ser Lys Gln Gln Ser
 245 250 255
 Ile Gln Glu Val Thr Trp Val Leu Leu Lys Ala Phe Ser Phe Ile Arg
 260 265 270
 Glu Ala Glu His Lys Ser Ser Glu Asn Leu His Pro Asp Asn Val Ile
 275 280 285
 Lys Lys Lys Asn Pro Phe Ser Glu Gly Lys Phe Lys Leu Ala Ala Glu
 290 295 300
 Ile Cys Ile Cys Asn Glu Glu Leu Asn Val Asn Pro Gln Asp Asn Gly
 305 310 315 320
 Glu Asn Ile Ser Trp Thr Cys Gln Arg Ser Ser Gln Gln Ser Ile Lys
 325 330 335
 Ser Leu Ala Trp Arg Pro Arg Arg Lys Trp Phe Cys Gly Thr Gly Pro
 340 345 350
 Gly Ser Leu Cys Cys Val Gln Pro Arg Asp Leu Val Pro Cys Val Pro
 355 360 365

Val Asn Ser Ala Val Ala Ser Glu Gly Ala Ser Pro Lys Pro Trp Gln
 370 375 380
 Leu Pro Ser Gly Val Glu Pro Val Gly Ala Lys Lys Ser Arg Ile Glu
 385 390 395 400
 Val Trp Glu Pro Pro Ile Arg Phe Gln Lys Ile Tyr Gly Asn Pro Trp
 405 410 415
 Met Pro Arg Gln Lys Phe Ala Val Gly Val Gly Ser Ser Trp Arg Thr
 420 425 430
 Ser Ala Arg Val Val Gln Lys Gly Asn Val Gly Trp Glu Pro Pro His
 435 440 445
 Arg Val Pro Ser Gly Ala Pro Ser Ser Arg Ala Val Arg Arg Ser Pro
 450 455 460
 Pro Ser Ser Arg Leu Gln Lys Gly Arg Ser Thr Asp Ser Leu Gln His
 465 470 475 480
 Val Pro Glu Lys Ser Thr Asp Thr Gln Cys Gln Pro Val Lys Ala Ala
 485 490 495
 Gly Met Glu Ser Val Pro Tyr Lys Thr Val Val Ala Glu Leu Thr Lys
 500 505 510
 Thr Val Gly Ile Tyr Leu Leu His Cys His Asp Leu Asp Val Arg His
 515 520 525
 Gly Val Lys Arg Asp His Phe Gly Ala Leu Arg Phe Asp Cys Pro Thr
 530 535 540
 Gly Phe Arg Thr Tyr Met Gly Pro Val Pro Leu Cys Phe Gly Gln Phe
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 Met

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 of SEQ ID N0:6

<221> misc_feature
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 <223> n = A,T,C or G

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